SEQUENCE LISTING

<110> Ehrhardt, Thomas
Sonnewald, Uwe
Bornke, Frederik
Chen, Shuai

<120> Sucrose-6-Phosphate Phosphatase as Target for Herbicides

<130> 532622010200

<140> Not yet assigned
<141> 2005-01-24

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 1278

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1)..(1275)

<223>

<400> 1

```
atg gat cag cta acc agt gcc gca cgt ctc atg ata gtc tca gat cta       48
Met Asp Gln Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
1               5                  10                  15

gac cat aca atg gta gat cat cat gat gcc gag aac ctt tct ctg ctt       96
Asp His Thr Met Val Asp His His Asp Ala Glu Asn Leu Ser Leu Leu
            20                  25                  30

aga ttt aat gct tta tgg gag gcg aat tat cgt gat aac tct ttg tta      144
Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser Leu Leu
        35                  40                  45

gtg ttc tca act ggg aga tca cct aca ctt tac aag gag ttg agg aaa      192
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
    50                  55                  60
```

```
gaa aag ccc atg cta acc cca gat att act att atg tcg gtg gga act      240
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
65                  70                  75                  80

gaa ata aca tat ggt aac tct gtg gtg cct gat gat ggt tgg gaa gct      288
Glu Ile Thr Tyr Gly Asn Ser Val Val Pro Asp Asp Gly Trp Glu Ala
                85                  90                  95

ttt cta aat aac aag tgg gac aga aag ata gta aca gag gag act agc      336
Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
            100                 105                 110

aag ttt cct gaa ctc act cta cag tca gaa acg gag cag cga cca cac      384
Lys Phe Pro Glu Leu Thr Leu Gln Ser Glu Thr Glu Gln Arg Pro His
        115                 120                 125

aag gtc agt ttc tat gtt cag aaa gac aaa gca caa gat ata atg aaa      432
Lys Val Ser Phe Tyr Val Gln Lys Asp Lys Ala Gln Asp Ile Met Lys
    130                 135                 140

act ctt tcc aag cgc ttc gaa gaa cgt ggg ctg gat gtc aaa ata att      480
Thr Leu Ser Lys Arg Phe Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
145                 150                 155                 160

tac agt gga ggc atg gat cta gat ata tta cca caa ggt gct ggc aaa      528
Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
                165                 170                 175

gga caa gca ctt gca tat ttg ctt aag aaa ttg aag agt gag gga aaa      576
Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
            180                 185                 190

tta cca aac aac acc ctt gcc tgt ggt gac tct ggg aat gat gct gag      624
Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
        195                 200                 205

cta ttc agt atc cca gat gtg tat ggt gta atg gta gct aat gca cag      672
Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
    210                 215                 220

gag gaa tta ttg caa tgg cat gct gca aat gcg aag aat aat cct aaa      720
Glu Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn Pro Lys
225                 230                 235                 240

gta att cat gca aca gag agg tgt gct gcc ggt atc ata caa gct att      768
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
                245                 250                 255

ggt cat tcc aac cta ggt cca agt acc tcc cct aga gat gtt atg gat      816
Gly His Ser Asn Leu Gly Pro Ser Thr Ser Pro Arg Asp Val Met Asp
            260                 265                 270

ttg tca gac tgc aag atg gag aac ttt gtt ccc gcc tat gaa gtt gtc      864
Leu Ser Asp Cys Lys Met Glu Asn Phe Val Pro Ala Tyr Glu Val Val
        275                 280                 285

aaa ttt tac cta ttt ttt gag aaa tgg agg cgt gga gaa att gag cat      912
Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu His
    290                 295                 300

tct gag cat tac ctg tca aac ctt aaa gca gtg tgt aga cca tct ggt      960
Ser Glu His Tyr Leu Ser Asn Leu Lys Ala Val Cys Arg Pro Ser Gly
305                 310                 315                 320
```

```
act ttt gtc cac cca tct ggt gtt gag aaa tcc ctc cag gaa tgt gta      1008
Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu Cys Val
                325                 330                 335

act tta ttc ggg aca tgt cat ggt gac aaa cag ggg aaa caa ttt cgt      1056
Thr Leu Phe Gly Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg
            340                 345                 350

att tgg gtc gat caa gtt tta cct gta cag gtt ggt tcg gac tca tgg      1104
Ile Trp Val Asp Gln Val Leu Pro Val Gln Val Gly Ser Asp Ser Trp
        355                 360                 365

tta gtg agt ttc aag aaa tgg gag ctc tct ggt gaa gac agg cga tgt      1152
Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Arg Arg Cys
    370                 375                 380

tgc ata act aca gtc cta tta agt tca aag aat aag act gtc gca gat      1200
Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val Ala Asp
385                 390                 395                 400

gga ctc act tgg acc cac gta cat cag aca tgg ctg aat gga gct gca      1248
Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Asn Gly Ala Ala
                405                 410                 415

gca agt gac tcc gcg tcc tgg ttc ttt tag                             1278
Ala Ser Asp Ser Ala Ser Trp Phe Phe
            420                 425
```

<210> 2

<211> 425

<212> PRT

<213> Nicotiana tabacum

<400> 2

```
Met Asp Gln Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
1               5                   10                  15

Asp His Thr Met Val Asp His His Asp Ala Glu Asn Leu Ser Leu Leu
            20                  25                  30

Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser Leu Leu
        35                  40                  45

Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
    50                  55                  60

Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
65                  70                  75                  80

Glu Ile Thr Tyr Gly Asn Ser Val Val Pro Asp Asp Gly Trp Glu Ala
```

85 90 95

Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
100 105 110

Lys Phe Pro Glu Leu Thr Leu Gln Ser Glu Thr Glu Gln Arg Pro His
115 120 125

Lys Val Ser Phe Tyr Val Gln Lys Asp Lys Ala Gln Asp Ile Met Lys
130 135 140

Thr Leu Ser Lys Arg Phe Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
145 150 155 160

Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
165 170 175

Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
180 185 190

Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
195 200 205

Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
210 215 220

Glu Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn Pro Lys
225 230 235 240

Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
245 250 255

Gly His Ser Asn Leu Gly Pro Ser Thr Ser Pro Arg Asp Val Met Asp
260 265 270

Leu Ser Asp Cys Lys Met Glu Asn Phe Val Pro Ala Tyr Glu Val Val
275 280 285

Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu His
290 295 300

Ser Glu His Tyr Leu Ser Asn Leu Lys Ala Val Cys Arg Pro Ser Gly
305 310 315 320

Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu Cys Val
325 330 335

Thr Leu Phe Gly Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg
340 345 350

Ile Trp Val Asp Gln Val Leu Pro Val Gln Val Gly Ser Asp Ser Trp
355 360 365

Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Arg Arg Cys
370 375 380

Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val Ala Asp
385 390 395 400

Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Asn Gly Ala Ala
405 410 415

Ala Ser Asp Ser Ala Ser Trp Phe Phe
420 425

<210> 3

<211> 1278

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1)..(1275)

<223>

<400> 3

atg gat cag cta acc agt gcc gca cgt ctc atg ata gtc tca gat ctt 48
Met Asp Gln Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
1 5 10 15

gac cat acc atg gtt gat cat cat gat cct gag aac ctt tct ctg ctt 96
Asp His Thr Met Val Asp His His Asp Pro Glu Asn Leu Ser Leu Leu
20 25 30

agg ttt aat gct tta tgg gag gcc aat tat cgt gaa aac tcc ttg tta 144
Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Glu Asn Ser Leu Leu
35 40 45

gtg ttc tca act ggg aga tca cct acc ctt tac aag gag ttg aga aaa 192
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
50 55 60

gag aag ccc atg cta acc cca gat att acc att atg tct gtg ggg act 240
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr

65 70 75 80

gaa ata act tat ggt aac tct atg gag cca gat gat ggt tgg gaa gca 288
Glu Ile Thr Tyr Gly Asn Ser Met Glu Pro Asp Asp Gly Trp Glu Ala
85 90 95

ttt tta aat gat aag tgg gat cgg aaa ata gtg aca gag gag aca agc 336
Phe Leu Asn Asp Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
100 105 110

aaa ttt cct gaa ctc acc ctt cag tca gaa aca gag cag cga cca cac 384
Lys Phe Pro Glu Leu Thr Leu Gln Ser Glu Thr Glu Gln Arg Pro His
115 120 125

aag gtc agt ttc tat gtt cag aaa gac aag gct caa gat ata acg gga 432
Lys Val Ser Phe Tyr Val Gln Lys Asp Lys Ala Gln Asp Ile Thr Gly
130 135 140

act ctt tcc aag cgc ttg gaa gaa cgt ggg ttg gat gtc aaa ata att 480
Thr Leu Ser Lys Arg Leu Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
145 150 155 160

tat agc gga ggg atg gat ttg gac att ttg cca caa ggt gct ggc aaa 528
Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
165 170 175

gga cga gca ctt gca tat ttg ctt aag aaa tta aag agt gag ggc aag 576
Gly Arg Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
180 185 190

tta cca aac aac acg ctt gcc tgt ggt gac tct gga aat gat gct gag 624
Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
195 200 205

ctt ttc agt atc cca gat gtt tat ggt gtg atg gta gcg aat gca cag 672
Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
210 215 220

gag gag tta tta caa tgg cgt gct gca aat gca aaa gat agt cca aaa 720
Glu Glu Leu Leu Gln Trp Arg Ala Ala Asn Ala Lys Asp Ser Pro Lys
225 230 235 240

gta att cat gca aca gag aga tgt gcc gcg ggt ata ata caa gca att 768
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
245 250 255

ggg cat ttc aac ctg gga cca aat acc tct cct aga gat gtt aca gat 816
Gly His Phe Asn Leu Gly Pro Asn Thr Ser Pro Arg Asp Val Thr Asp
260 265 270

atg tca gac tgc aag atg gag aat ttt gtt cct gct tat gaa gtc gtc 864
Met Ser Asp Cys Lys Met Glu Asn Phe Val Pro Ala Tyr Glu Val Val
275 280 285

aaa ttt tac ttg ttt ttc gag aaa tgg agg cgt gga gaa att gag aat 912
Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu Asn
290 295 300

tct gac ctt cac ttg tca aac ctg aaa gca gtt tgt aga cca tcc ggt 960
Ser Asp Leu His Leu Ser Asn Leu Lys Ala Val Cys Arg Pro Ser Gly
305 310 315 320

act ttt gtg cac cca tct gga gtt gag aaa tat ctt gag gac tgc ata 1008

```
Thr Phe Val His Pro Ser Gly Val Glu Lys Tyr Leu Glu Asp Cys Ile
                325                 330                 335

aat aca ttg aga act tgt cac ggt gac aaa cag ggt aaa caa ttt cgt     1056
Asn Thr Leu Arg Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg
            340                 345                 350

att tgg gtt gat cta gtg tta cct aca cag gtt ggt tca gat tca tgg     1104
Ile Trp Val Asp Leu Val Leu Pro Thr Gln Val Gly Ser Asp Ser Trp
        355                 360                 365

tta gtg agt ttc aag aaa tgg gag ctt tgt ggc gaa gag cga caa tgt     1152
Leu Val Ser Phe Lys Lys Trp Glu Leu Cys Gly Glu Glu Arg Gln Cys
    370                 375                 380

tgc ata act act gtc ttg tta agt tca aag aat gtg acg gtc gcg gat     1200
Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Val Thr Val Ala Asp
385                 390                 395                 400

ggg ctc act tgg aca cat gtg cat cag act tgg ctg cag gga gca gca     1248
Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Gln Gly Ala Ala
                405                 410                 415

gca agt gac tcc gcg tcc tgg ttc ttt taa                            1278
Ala Ser Asp Ser Ala Ser Trp Phe Phe
            420                 425
```

<210> 4

<211> 425

<212> PRT

<213> Nicotiana tabacum

<400> 4

```
Met Asp Gln Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
1               5                   10                  15

Asp His Thr Met Val Asp His His Asp Pro Glu Asn Leu Ser Leu Leu
            20                  25                  30

Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Glu Asn Ser Leu Leu
        35                  40                  45

Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
    50                  55                  60

Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
65                  70                  75                  80

Glu Ile Thr Tyr Gly Asn Ser Met Glu Pro Asp Asp Gly Trp Glu Ala
                85                  90                  95
```

```
Phe Leu Asn Asp Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
            100                 105                 110

Lys Phe Pro Glu Leu Thr Leu Gln Ser Glu Thr Glu Gln Arg Pro His
        115                 120                 125

Lys Val Ser Phe Tyr Val Gln Lys Asp Lys Ala Gln Asp Ile Thr Gly
    130                 135                 140

Thr Leu Ser Lys Arg Leu Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
145                 150                 155                 160

Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
                165                 170                 175

Gly Arg Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
            180                 185                 190

Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
        195                 200                 205

Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
    210                 215                 220

Glu Glu Leu Leu Gln Trp Arg Ala Ala Asn Ala Lys Asp Ser Pro Lys
225                 230                 235                 240

Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
                245                 250                 255

Gly His Phe Asn Leu Gly Pro Asn Thr Ser Pro Arg Asp Val Thr Asp
            260                 265                 270

Met Ser Asp Cys Lys Met Glu Asn Phe Val Pro Ala Tyr Glu Val Val
        275                 280                 285

Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu Asn
    290                 295                 300

Ser Asp Leu His Leu Ser Asn Leu Lys Ala Val Cys Arg Pro Ser Gly
305                 310                 315                 320

Thr Phe Val His Pro Ser Gly Val Glu Lys Tyr Leu Glu Asp Cys Ile
                325                 330                 335

Asn Thr Leu Arg Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg
            340                 345                 350
```

Ile Trp Val Asp Leu Val Leu Pro Thr Gln Val Gly Ser Asp Ser Trp
355 360 365

Leu Val Ser Phe Lys Lys Trp Glu Leu Cys Gly Glu Glu Arg Gln Cys
370 375 380

Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Val Thr Val Ala Asp
385 390 395 400

Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Gln Gly Ala Ala
405 410 415

Ala Ser Asp Ser Ala Ser Trp Phe Phe
420 425

<210> 5

<211> 1642

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (70)..(1344)

<223>

<400> 5
acacaaaaaa gatttcattt ttttgtttcc ccaattccca tttcaggttg aagccaattt 60

acatcaatc atg gat cgg cta acc agt gct gca cgt ctc atg ata gtc tca 111
Met Asp Arg Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser
1 5 10

gat ctt gac cat aca atg gta gat cat cac gat tcc gag aac ctt tct 159
Asp Leu Asp His Thr Met Val Asp His His Asp Ser Glu Asn Leu Ser
15 20 25 30

ctg ctt agg ttc aat gct tta tgg gaa gcc aat tat cgt gat aac tct 207
Leu Leu Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser
35 40 45

ttg tta gtg ttc tct act ggg aga tca cct aca ctt tac aag gaa tta 255
Leu Leu Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu
50 55 60

agg aaa gaa aag ccc atg cta acc cca gat att aca att atg tct gtg 303
Arg Lys Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val

```
        65                  70                  75

gga act gaa ata aca tat ggt aac gct atg gtg cct gat gat ggt tgg      351
Gly Thr Glu Ile Thr Tyr Gly Asn Ala Met Val Pro Asp Asp Gly Trp
    80                  85                  90

gaa aca ttt ctg aat aac aag tgg gat aga aag ata gta aca gag gag      399
Glu Thr Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu
95                  100                 105                 110

aca agc aag ttt cct gaa ctc agt ctg cag tca gaa aca gag cag cga      447
Thr Ser Lys Phe Pro Glu Leu Ser Leu Gln Ser Glu Thr Glu Gln Arg
                115                 120                 125

cca cac aag gtc agt ttc tat gtt cag aaa gag aaa gct caa gat ata      495
Pro His Lys Val Ser Phe Tyr Val Gln Lys Glu Lys Ala Gln Asp Ile
            130                 135                 140

atg aaa act ctt tcc aag cgc ttg gaa gaa cgt ggg ctg gat gtc aaa      543
Met Lys Thr Leu Ser Lys Arg Leu Glu Glu Arg Gly Leu Asp Val Lys
        145                 150                 155

ata att tac agt gga ggg atg gat cta gat ata tta cca cag ggt gct      591
Ile Ile Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala
    160                 165                 170

ggc aaa gga caa gca ctt gca tat ctg ctt aag aaa ctg aag agc gag      639
Gly Lys Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu
175                 180                 185                 190

gga aaa tta cca agc aac acc ctt gcc tgc ggc gac tcc ggg aat gac      687
Gly Lys Leu Pro Ser Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp
                195                 200                 205

gct gaa tta ttc agt atc cca gat gtg tat ggt gta atg gta gct aat      735
Ala Glu Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn
            210                 215                 220

gcg cag aag gaa tta ctg cag tgg cat gct gca aat gca aaa aat aat      783
Ala Gln Lys Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn
        225                 230                 235

ccc aaa gta att cat gca tca gag agg tgt gcc gcc ggt atc ata caa      831
Pro Lys Val Ile His Ala Ser Glu Arg Cys Ala Ala Gly Ile Ile Gln
    240                 245                 250

gcc att ggt cat ttc aaa cta ggt cca agt acc tcc cca aga gac gtt      879
Ala Ile Gly His Phe Lys Leu Gly Pro Ser Thr Ser Pro Arg Asp Val
255                 260                 265                 270

acg gat ttg tca gat tgc aag atg gac aac ttt gtt cct gcc tat gaa      927
Thr Asp Leu Ser Asp Cys Lys Met Asp Asn Phe Val Pro Ala Tyr Glu
                275                 280                 285

gtt gtc aaa ttt tac ctg ttt ttt gag aaa tgg agg cgt gga gaa att      975
Val Val Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile
            290                 295                 300

gag cat tct gag cat tat ctg cca aac ctg aaa gca gtg tgt ata cca     1023
Glu His Ser Glu His Tyr Leu Pro Asn Leu Lys Ala Val Cys Ile Pro
        305                 310                 315

tct ggt act ttt gtt cac cca tct ggt gtt gag aaa tcc ctt cag gaa     1071
```

```
Ser Gly Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu
    320                 325                 330

tgt gta act tca ttc gga aca tgt cat gct gac aag cag ggg aaa caa     1119
Cys Val Thr Ser Phe Gly Thr Cys His Ala Asp Lys Gln Gly Lys Gln
335                 340                 345                 350

tat cgt gtt tgg gtc gat caa gtt tta cct tca cag gtt ggt tca gac     1167
Tyr Arg Val Trp Val Asp Gln Val Leu Pro Ser Gln Val Gly Ser Asp
                355                 360                 365

tca tgg tta gtg agt ttc aag aag tgg gag ctc tct ggt gaa gac atg     1215
Ser Trp Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Met
            370                 375                 380

cga tgc tgc ata acc aca gtc cta tta agt tca aag aat aag act gtt     1263
Arg Cys Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val
        385                 390                 395

gca gac ggg ctc act tgg act cac gta cat cag aca tgg ctg cac ggt     1311
Ala Asp Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu His Gly
    400                 405                 410

gat gca gca agt gac tcc gca acc tgg ttc ttt tagattgtca tctcagtgta   1364
Asp Ala Ala Ser Asp Ser Ala Thr Trp Phe Phe
415                 420                 425

ttaactctga aaattccgca ccccttttac cagttcacac ccagaataaa cacaacatac   1424

aaactatagt tgataatcaa tgtattaact ttctccttct ttgataatca atgtattgcc   1484

atctaaacca gtgaagatgg ctttatcttt tgtgtagtat aaagaattat attagtatca   1544

tagttgttct tgtatttgat tcagaattca agatgagatt gttgcaaatt gctgcatatt   1604

taagtttcca aaaaaaaaaa aaaaaaaaaa aaaaaaaa                           1642
```

<210> 6

<211> 425

<212> PRT

<213> Solanum tuberosum

<400> 6

```
Met Asp Arg Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
1               5                   10                  15

Asp His Thr Met Val Asp His His Asp Ser Glu Asn Leu Ser Leu Leu
            20                  25                  30

Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser Leu Leu
        35                  40                  45

Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
```

50 55 60

Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
65 70 75 80

Glu Ile Thr Tyr Gly Asn Ala Met Val Pro Asp Asp Gly Trp Glu Thr
85 90 95

Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
100 105 110

Lys Phe Pro Glu Leu Ser Leu Gln Ser Glu Thr Glu Gln Arg Pro His
115 120 125

Lys Val Ser Phe Tyr Val Gln Lys Glu Lys Ala Gln Asp Ile Met Lys
130 135 140

Thr Leu Ser Lys Arg Leu Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
145 150 155 160

Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
165 170 175

Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
180 185 190

Leu Pro Ser Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
195 200 205

Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
210 215 220

Lys Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn Pro Lys
225 230 235 240

Val Ile His Ala Ser Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
245 250 255

Gly His Phe Lys Leu Gly Pro Ser Thr Ser Pro Arg Asp Val Thr Asp
260 265 270

Leu Ser Asp Cys Lys Met Asp Asn Phe Val Pro Ala Tyr Glu Val Val
275 280 285

Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu His
290 295 300

Ser Glu His Tyr Leu Pro Asn Leu Lys Ala Val Cys Ile Pro Ser Gly
305 310 315 320

Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu Cys Val
325 330 335

Thr Ser Phe Gly Thr Cys His Ala Asp Lys Gln Gly Lys Gln Tyr Arg
340 345 350

Val Trp Val Asp Gln Val Leu Pro Ser Gln Val Gly Ser Asp Ser Trp
355 360 365

Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Met Arg Cys
370 375 380

Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val Ala Asp
385 390 395 400

Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu His Gly Asp Ala
405 410 415

Ala Ser Asp Ser Ala Thr Trp Phe Phe
420 425

<210> 7

<211> 199

<212> DNA

<213> Solanum tuberosum

<400> 7
gtacggaccg tactactcta ttcgtttcaa tatatttatt tgtttcagct gactgcaaga 60

ttcaaaaatt tctttattat tttaaatttt gtgtcactca aaaccagata aacaatttga 120

tatagagcca ctatatatat acatattctc gattatatat gtaaatgagt tacccttttt 180

ttccacttaa attatatag 199

<210> 8

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 8
atggatcagc taaccagtcg ccgcac 26

<210> 9

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 9
ctaaaagaac caggacgcgg agtcact 27

<210> 10

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 10
cctgcaggct cgagactagt agatctggta cggaccgtac tactcta 47

<210> 11

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 11
cctgcagggt cgactctaga ggatccccta tataatttaa gtggaaaa 48

<210> 12

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 12
ggatccatgg atcagctaac cagtgcc 27

<210> 13

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 13
gtcgactacc attacaccat aacacatc 28

<210> 14

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence

<400> 14
gttagtgttc tcaactggga gatcacc 27

<210> 15

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 15
cccatttctt gaaactcact aaccatga 28

<210> 16

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 16
atggcagacg gtgaggatat tca 23

<210> 17

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 17
gcctttgcaa tccacatctg ttg 23

<210> 18

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 18
ggatccatgg atcagctaac cagtgcc 27

<210> 19

Sequence listing

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 19
gtcgacctaa aagaaccagg acgcggagtc act 33